Inheritance of Type I glandular trichomes in *Cucumis melo*

F.J. Palomares-Rius, E. Sarria, J.M. Alba, and M.L. Gómez-Guillamón

Experimental Station ‘La Mayora’, CSIC, 29750, Algarrobo-Costa (Málaga- Spain)

* Corresponding author e-mail: guillamon@eelm.csic.es

**Keywords:** *Aphis gossypii*, antixenosis, heritability, genetic model, additive, dominance, epistasis

**Abstract**

A high density of glandular trichomes of Type I could contribute to enhance resistance to *Aphis gossypii* in melon breeding programs with the *Vat* gene. To study the inheritance of this trait, a six-generation genetic family was obtained from the cross between the accession TGR-1551, with high density of glandular trichomes and the Spanish cultivar ‘Bola de oro’ with low trichome density. The genetic model estimated showed that the Type I trichome density followed an oligogenic inheritance with important additive effect and strong epistatic effect between heterozygous loci. The values for broad sense heritability ($H^2$) and narrow sense heritability ($h^2$) were 0.86 and 0.50, respectively, which made this character suitable for breeding.

**INTRODUCTION**

Many reports have revealed the importance of glandular trichomes against plant pests (Khan et al. 2000; Bahlmann et al. 2003; Kennedy 2003; Wagner et al. 2004; Simmons and Gurr 2005; Simmons et al. 2003, 2005). The presence of different types of glandular trichomes in Cucurbitaceae species were reported by Kolb and Müller (2004). Type I glandular trichomes were firstly described in *Cucumis melo* by Gómez-Guillamón et al. (2006). More recently, Sarria et al. (2007) suggested that these trichomes were involved in the early rejection of melon plants as hosts by *Aphis gossypii* Glover, and, in high density, they could be considered as an additional factor to the aphid resistance controlled by the *Vat* gene. Knowledge of the inheritance of density of Type I glandular trichomes in melon will enhance their utilization in breeding for resistance to *A. gossypii*. Genetics of this trait was studied by crossing the aphid resistant accession TGR-1551, with high density of glandular trichomes, and the Spanish cultivar ‘Bola de oro’, susceptible to aphids and with low trichome density.

**MATERIALS AND METHODS**

Trichome density was evaluated in a six-generation family, obtained from the cross TGR-1551 x ‘Bola de oro’, consisting of the two parents, the F1, the F2 and the two first backcrosses. The number of plants tested for each generation is shown in Figure 1. Plants were grown until 8-10 true leaf stage in pots (500 cm³) filled with soil substrate placed in a growth chamber at 25°C (light) and 20°C (dark) with a 16:8 h (L:D) photoperiod. Two disks (5.9 mm diameter) from the second leaf from apex were taken per plant. Leaf disks were decolorated by heating to 80°C for three
minutes in 100 % ethanol. Samples were stained with an aqueous solution containing 0.05 % toluidine blue O (O’Brien et al. 1964). Glandular trichomes were inspected and counted under microscope at 400x.

The average of the number of trichomes counted in the two leaf disks was considered as the phenotypic value of plants. Trichome density data were transformed by log (x+1) prior to data analysis.

The midparent value (m), together with gene effects of additive (d), dominance (h), and digenic epistatic interaction components of means for Type I trichome density were estimated following methods by Mather and Jinks (1982). The adequacies of additive-dominance models, with and without digenic epistatic interactions, were tested by the joint scaling tests.

The minimum number of genetic factors involved in the inheritance of the character was estimated by Wright’s formula using the F2 segregation. The genotypic range needed for Wright’s formula was determined by the difference between the parental means (assuming that all factors with positive additive effects are present in one parent), and using the phenotypic range of the segregating population (both parental lines can contribute with positive additive factors to the trait) (Bjarko and Line 1988).

The values for broad sense heritability (H2) and narrow sense heritability (h2) were calculated in a single plant basis following Rodriguez-Herrera et al. (2000) and Warner (1952), respectively.

Figure 1. Frequency distributions of Type I glandular trichome density in the six generations of Cucumis melo from the cross TGR-1551 x ‘Bola de oro’. Number of plants (n), mean (µ), and standard deviation (σ).
RESULTS AND DISCUSSION

Type I glandular trichome density distributions of both parents did not overlap, the F1 performed like TGR-1551 and F2 and backcrosses showed wide segregations (Fig. 1). Segregation of F2 generation, with most plants showing low trichome densities, was unexpected from the apparently dominant mode of inheritance of the trait inferred from F1 performance. Since trichome densities on plants from segregating generations did not separate into discrete classes, a quantitative rather than a Mendelian approach has been used to study the genetic control of the character.

Quantitative data analysis by joint-scaling tests fitted with some of the genetic models assayed (Tab. 1). It is noteworthy that the values of additive component in all models were very similar, \([d] = 0.34\). Nevertheless, the models with maximum likelihood were those where epistatic dominance x dominance effect \([l]\) was included, especially \(mdhil\) (Tab. 1). In this model the dominance component \([h]\) was not significant and the model could explain the similar-to-TGR-1551 parent performance of F1 generation by a positive, strong epistatic effect of heterozygous loci.

The minimum number of genetic factors \((n_e)\) estimated according to Wright’s formula pointed to a monogenic control \((n_e = 0.844 \pm 0.125)\). Thereby, TGR-1551 would contribute with a major locus to higher trichome density. However, according to the modifications described by Bjarko and Line (1988), the minimum number of genetic factors estimated suggested that Type I trichome density may be rather an oligogenic character \((n_e = 2.840 \pm 0.375)\). The higher \(n_e\) value so estimated, using the F2 phenotypic range as estimator of genotypic range, showed that ‘Bola de oro’ parent may also contribute to higher trichome density with additional genes.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>(mdh)</th>
<th>(mdhi)</th>
<th>(mdhl)</th>
<th>(mdhij)</th>
<th>(mdhil)</th>
<th>(mdhil)</th>
<th>(mdhjl)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(m)</td>
<td>2.28</td>
<td>2.24</td>
<td>2.28</td>
<td>2.29</td>
<td>2.25</td>
<td>2.48</td>
<td>2.29</td>
</tr>
<tr>
<td></td>
<td>±0.01</td>
<td>±0.04</td>
<td>±0.12</td>
<td>±0.01</td>
<td>±0.04</td>
<td>±0.11</td>
<td>±0.01</td>
</tr>
<tr>
<td>([d])</td>
<td>0.34</td>
<td>0.34</td>
<td>0.34</td>
<td>0.34</td>
<td>0.34</td>
<td>0.34</td>
<td>0.34</td>
</tr>
<tr>
<td></td>
<td>±0.01</td>
<td>±0.01</td>
<td>±0.01</td>
<td>±0.01</td>
<td>±0.01</td>
<td>±0.01</td>
<td>±0.01</td>
</tr>
<tr>
<td>([h])</td>
<td>0.29</td>
<td>0.34</td>
<td>0.30</td>
<td>0.17</td>
<td>0.33</td>
<td>-0.30</td>
<td>0.18</td>
</tr>
<tr>
<td></td>
<td>±0.02</td>
<td>±0.05</td>
<td>±0.02</td>
<td>±0.07</td>
<td>±0.05</td>
<td>±0.28</td>
<td>±0.07</td>
</tr>
<tr>
<td>([i])</td>
<td>0.05</td>
<td>0.04</td>
<td>0.19</td>
<td>±0.04</td>
<td>±0.05</td>
<td>±0.11</td>
<td></td>
</tr>
<tr>
<td>([j])</td>
<td>-0.08</td>
<td>-0.07</td>
<td>-0.04</td>
<td>±0.08</td>
<td>±0.08</td>
<td>±0.08</td>
<td></td>
</tr>
<tr>
<td>([l])</td>
<td>0.13</td>
<td>0.40</td>
<td>0.12</td>
<td>±0.07</td>
<td>±0.18</td>
<td>±0.07</td>
<td></td>
</tr>
<tr>
<td>(\chi^2)</td>
<td>6.26</td>
<td>5.23</td>
<td>5.33</td>
<td>2.87</td>
<td>4.54</td>
<td>0.00</td>
<td>2.64</td>
</tr>
<tr>
<td></td>
<td>(3 df)</td>
<td>(2 df)</td>
<td>(2 df)</td>
<td>(2 df)</td>
<td>(1 df)</td>
<td>(1 df)</td>
<td>(1 df)</td>
</tr>
<tr>
<td>(P)</td>
<td>0.100</td>
<td>0.073</td>
<td>0.070</td>
<td>0.238</td>
<td>0.033</td>
<td>0.973</td>
<td>0.104</td>
</tr>
</tbody>
</table>

* Parameter different from 0 according to t-distribution test \((P \leq 0.05)\); df, degrees of freedom. \(m\) = midpoint between parent; \([d]\) = additive component; \([h]\) = dominance component; \([i]\) = additive x additive interaction component; \([j]\) = additive x dominance interaction component; \([l]\) = dominance x dominance interaction component.
High value of broad sense heritability ($H^2 = 0.861$) and moderate value for narrow sense heritability ($h^2 = 0.505$) were estimated for glandular trichome density. Heritability is an important parameter to be considered in the introgression of quantitative traits. These values showed the importance of genotypic and mainly of additive factors in the inheritance of the glandular trichome density. It anticipates success in introgression and selection melon programs for similar vegetal materials and similar environmental conditions.

Leaves with high density of trichomes of Type I will reinforce the aphid control in melon genotypes carrying the $Vat$ gene. Since these trichomes were always observed in high numbers in wild melon types and in low numbers in bred material (Sarria et al. 2007), their density may have been linked to genes for undesirable agronomical melon traits. Studies have to be done to know whether or not this character is associated with undesirable characters which could difficult its introduction in commercial material (Alvarez et al. 2006).

Further genetic analysis will be carried out using a RIL population generated from the original cross TGR-1551 x ‘Bola de oro’ in order to identify QTLs for trichome density.

ACKNOWLEDGEMENTS

The authors thank the valuable contribution of Dr. R. Fernández-Muñoz to improve statistical analysis and the collaboration of R. Tobar and R. Camero in all the experiments. This work has been financed by the CICYT Research Project: AGL2005-03850-C02-01.

Literature Cited


O’Brien TP, Feder N, McCully M (1964) Polychromatic staining of plant cell walls by toluidine blue. Protoplasma 59:367-373